

GaMYB1\_alignment\_and\_sequence.txt

Exhibit 2

gi|7438345|pir||T09879 myb-related protein A - upland cotton  
gi|437327|gb|AAA33067.1| MYB1 [Gossypium hirsutum]  
gi|23476277|gb|AAN28269.1| myb-like transcription factor 1 [Gossypium hirsutum]

Length = 294  
Score = 602 bits (1553), Expect = e-171  
Identities = 288/294 (97%), Positives = 291/294 (98%)  
Frame = +3

Query: 144 MGRSPCCEKAHTNKGAWTKEEDQRLINIRVHGEWCWRS LPAAGLLRCGKSCRLRWINY 323  
Sbjct: 1 MGRSPCCEKAHTNKGAWTKEEDQRLINIRVHGEWCWRS LPAAGLLRCGKSCRLRWINY 60  
Query: 324 LRPDLKRGNFTEEEDELI IKLHSL LGNKWSLIAGRLPGR TDNEIKNYWNTHIKRKLISRG 503  
Sbjct: 61 LRPDLKRGNFTEEEDELI IKLHSL LGNKWSLIAGRLPGR TDNEIKNYWNTHIKRKLISRG 120  
Query: 504 IDPQTHRPLNQTAITNTVTGPTELDFRNSPTSVSKSSSIKNPSLDFNYNEFHFKSHTDSL 683  
Sbjct: 121 IDPQTHRPLNQTAITNTVTGPTELDFRNSPTSVSKSSSIKNPSLDFNYNEFHFKSHTDSL 180  
Query: 684 EEPNCTASTGMTTDEEQEQLHKKQYGPSNGQDINLELSIGIVSADSSRVSSANSAESK 863  
Sbjct: 181 EEPNCTASTGMTTDEEQEQLHKKQYGPSNGQDINLELSIGIVSADSSRVSSANSAESK 240  
Query: 864 PKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYCYRPLDS 1025  
Sbjct: 241 PKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYCYRPLDS 294

>Contig20 GaMYB1  
GGCACGAGACAGTTTCTCTTTTTTGCTCATTTCCATCATCCCCATGTCCC  
CTCTCCATGTTTTCTAAATCTCTCCATATACCTATAACACCGTTATTCT  
TTCTCTATTCTACCTGATTTGATTTGATTTGATTTGTAAGTATGTTGGAC  
GATCACCTTGTGTGAAAAGGCTCATACCAACAAAGGTGCCTGGACCAA  
GAGGAAGATCAACGCCTCATCAACTACATCCGTGTCCATGGTGAAGGCTG  
CTGGCGTTCCCTCCCCAAAGCTGCTGGGCTGCTTAGATGTGGTAAGAGTT  
GCAGATTAAGATGGATAAACTACTTGAGGCCTGATCTTAAGAGAGGAAAT  
TTCAGTGAAGAAGAAGATGAGCTTATCATCAAGCTTCACAGTTTACTTGG  
AAACAAATGGTCATTGATTGCTGGAAGATTACCAGGAAGGACAGATAATG  
AGATAAAGAACTACTGGAACACACACATCAAAAGAAAGCTTATAAGCAGA  
GGAATTGATCCACAACTCATCGTCTCTCAATCAAACGGCCATTACCAA  
CACAGTCACAGGCCCCACCGAATTGGATTTAGAAAACCTCGCCACATCCG  
TTTCCAAATCCAGTTCCATCAAAAACCCGTCTCTGGATTTCAATTACAAT  
GAATTTCAATTTCAAGTCCCACACAGATTCCCTTGAAGAACCCAACTGTAC  
AGCCAGCACTGGCATGACTACAGATGAAGAACAACAAGAACAGCTGCACA  
AGAAGCAGCAATACGGTCCGAGCAATGGGCAAGACATAAATTTGGAGCTG  
TCGATTGGGATTGTTTCAGCTGACTCATCTCGGGTATCAAGTGCCAACTC  
GGCCGAGTCGAAACCAAGGTAGATAACAACAATTTCCAGTTTCTTGAAC  
AAGCTATGGTGGCTAAGGCGGTATGTTTGTGTTGGCAATTAGGTTTTGGA  
ACAAGTGAATTTGTAGGAACTGTCAAAATTCAAATTCAAATGGCTTCTA  
TAGTTATTGTAGACCTTGGATTATAGGGTCATCTTTTCTTCTTTCTT  
TCTGTTTTTAGGAGATAAATTAATTTCTAATTTATTTATCTTTTGCCTGCC  
CACTGTAATCAAAGCAAAATTATAAAACAAAGACTCTTTTGTATTTGTTT  
AATTTATAGGTTCAAAAAAAAAAAAAAAAAAAAA

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>Contig20\_Frame+3 GaMYB1

HETVSLFCSFPSSPCPLSMFF\*ISPYTYNTVILSLFYLI\*FDLIL\*LMGRSPCCEKAHTN  
KGAWTKEEDQRLINYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINYLRPDLKRGNFTEE  
EDELIIKLHSLLGKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRGIDPQTHRPLNQTA  
ITNTVTGPTELDFRNSPTSVSKSSSIKNPSLDFNYNEFHFKSHTDSLEEPNCTASTGMTT  
DEEQEQLHKKQYGPSNGQDINLELSIGIVSADSSRVSSANSAESKPKVDNNNFQFLEQ  
AMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS\*GHLFLLSFCF\*EIN\*FLI  
IIFLPAHCNQSKIIKQRLFLICSIYRFKKKKKK

>GaMYB1 - putative from GhMYB1 alignment

MGRSPCCEKAHTNKGAWTKEEDQRLINYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINY  
LRPDLKRGNFTEEEDELIIKLHSLLGKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRG  
IDPQTHRPLNQTAITNTVTGPTELDFRNSPTSVSKSSSIKNPSLDFNYNEFHFKSHTDSL  
EEPNCTASTGMTTDEEQEQLHKKQYGPSNGQDINLELSIGIVSADSSRVSSANSAESK  
PKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS